

SEQUENCE LISTING

<110> Negulescu, Paul
 Offermanns, Stefan
 Simon, Melvin
 Zuker, Charles

<120> PROMISCUOUS G-PROTEINS COMPOSITIONS AND THEIR USE

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 <141> 1997-06-19

<150> US 60/020,234
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Val Tyr Tyr Leu Ser His Leu Glu Arg Ile Thr Glu Glu Gly Tyr Val		
165 170 175		
cc ^c a ^c g ^c t ^a c ^a g ^g g ^t c ^t c ^g a ^g c ^g a ^t g ^c c ^c a ^c a ^c t ^g g ^g c ^a t ^c		576
Pro Thr Ala Gln Asp Val Leu Arg Ser Arg Met Pro Thr Thr Gly Ile		
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 Gly Pro Gly Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln Met Arg Ile
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Glu Glu Lys Thr Ala Ala Arg Ile Asp Gln Glu Ile Asn Arg Ile Leu																																																																																	
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Asn Val Ile Ala Leu Ile Tyr Leu Ala Ser Leu Ser Glu Tyr Asp Gln																																																																																	
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SEQUENCE ID LISTING

Nucleotide and Amino Acid Sequences of $\text{G}\alpha 15$

(SEQ ID NO: 2 and SEQ ID NO: 4, respectively)

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Phe Glu Lys Pro Tyr Ala Val Ala Met Gln Tyr Leu Trp Arg Asp Ala Gly Ile

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Arg Ala Cys Tyr Glu Arg Arg Glu Phe His Leu Leu Asp Ser Ala Val Tyr

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Tyr Leu Ser His Leu Glu Arg Ile Ser Glu Asp Ser Tyr Ile Pro Thr Ala Gln

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Glu Ser Leu Ala Leu Phe Ser Thr Ile Leu Glu Leu Pro Trp Phe Lys Ser Thr					
819	828	837	846	855	864
TCG GTC ATC CTC TTC CTC AAC AAG ACG GAC ATC CTG GAA GAT AAG ATT CAC ACC					

Ser Val Ile Leu Phe Leu Asn Lys Thr Asp Ile Leu Glu Asp Lys Ile His Thr					
873	882	891	900	909	918
TCC CAC CTG GCC ACA TAC TTC CCC AGC TTC CAG GGA CCC CGG CGA GAC GCA GAG					

Ser His Leu Ala Thr Tyr Phe Pro Ser Phe Gln Gly Pro Arg Arg Asp Ala Glu					
927	936	945	954	963	972
GCC GCC AAG AGC TTC ATC TTG GAC ATG TAT GCG CGC GTG TAC GCG AGC TGC GCA					

Ala Ala Lys Ser Phe Ile Leu Asp Met Tyr Ala Arg Val Tyr Ala Ser Cys Ala					
981	990	999	1008	1017	1026
GAG CCC CAG GAC GGT GGC AGG AAA GGC TCC CGC GCG CGC CGC TTC TTC GCA CAC					

Glu Pro Gln Asp Gly Gly Arg Lys Gly Ser Arg Ala Arg Arg Phe Phe Ala His					

1035 1044 1053 1062 1071 1080
TTC ACC TGT GCC ACG GAC ACG CAA AGC GTC CGC AGC GTG TTC AAG GAC GTG CGG
- - - - -
Phe Thr Cys Ala Thr Asp Thr Gln Ser Val Arg Ser Val Phe Lys Asp Val Arg

1089 1098 1107 1116 1125
GAC TCG GTG CTG GCC CGG TAC CTG GAC GAG ATC AAC CTG CTG TGA
- - - - -
Asp Ser Val Leu Ala Arg Tyr Leu Asp Glu Ile Asn Leu Leu ***

Nucleotide and Amino Acid Sequences of G 16
(SEQ ID NO: 1 and SEQ ID NO: 3, respectively)

9 18 27 36 45 54
ATG GCC CGC TCG CTG ACC TGG CGC TGC TGC CCC TGG TGC CTG ACG GAG GAT GAG
- - - - -
Met Ala Arg Ser Leu Thr Trp Arg Cys Cys Pro Trp Cys Leu Thr Glu Asp Glu

63 72 81 90 99 108
AAG GCC GCC CGC CGG GTG GAC CAG GAG ATC AAC AGG ATC CTC TTG GAG CAG AAG
- - - - -
Lys Ala Ala Ala Arg Val Asp Gln Glu Ile Asn Arg Ile Leu Leu Glu Gln Lys

117 126 135 144 153 162
AAG CAG GAC CGC GGG GAG CTG AAG CTG CTG CTT TTG GGC CCA GGC GAG AGC GGG
- - - - -
Lys Gln Asp Arg Gly Glu Leu Lys Leu Leu Leu Gly Pro Gly Glu Ser Gly

171 180 189 198 207 216
AAG AGC ACC TTC ATC AAG CAG ATG CGG ATC ATC CAC GGC GCC GGC TAC TCG GAG
- - - - -
Lys Ser Thr Phe Ile Lys Gln Met Arg Ile Ile His Gly Ala Gly Tyr Ser Glu

225 234 243 252 261 270

GAG GAG CGC AAG GGC TTC CGG CCC CTG GTC TAC CAG AAC ATC TTC GTG TCC ATG

Glu Glu Arg Lys Gly Phe Arg Pro Leu Val Tyr Gln Asn Ile Phe Val Ser Met

279 288 297 306 315 324
CGG GCC ATG ATC GAG GCC ATG GAG CGG CTG CAG ATT CCA TTC AGC AGG CCC GAG

Arg Ala Met Ile Glu Ala Met Glu Arg Leu Gln Ile Pro Phe Ser Arg Pro Glu

333 342 351 360 369 378
AGC AAG CAC CAC GCT AGC CTG GTC ATG AGC CAG GAC CCC TAT AAA GTG ACC ACG

Ser Lys His His Ala Ser Leu Val Met Ser Gln Asp Pro Tyr Lys Val Thr Thr

387 396 405 414 423 432
TTT GAG AAG CGC TAC GCT GCG GCC ATG CAG TGG CTG TGG AGG GAT GCC GGC ATC

Phe Glu Lys Arg Tyr Ala Ala Ala Met Gln Trp Leu Trp Arg Asp Ala Gly Ile

441 450 459 468 477 486
CGG GCC TGC TAT GAG CGT CGG CGG GAA TTC CAC CTG CTC GAT TCA GCC GTG TAC

Arg Ala Cys Tyr Glu Arg Arg Glu Phe His Leu Leu Asp Ser Ala Val Tyr

495 504 513 522 531 540
TAC CTG TCC CAC CTG GAG CGC ATC ACC GAG GAG GGC TAC GTC CCC ACA GCT CAG

Tyr Leu Ser His Leu Glu Arg Ile Thr Glu Glu Gly Tyr Val Pro Thr Ala Gln

549 558 567 576 585 594
GAC GTG CTC CGC AGC CGC ATG CCC ACC ACT GGC ATC AAC GAG TAC TGC TTC TCC

Asp Val Leu Arg Ser Arg Met Pro Thr Thr Gly Ile Asn Glu Tyr Cys Phe Ser

603 612 621 630 639 648
GTG CAG AAA ACC AAC CTG CGG ATC GTG GAC GTC GGG GGC CAG AAG TCA GAG CGT

Val Gln Lys Thr Asn Leu Arg Ile Val Asp Val Gly Gly Gln Lys Ser Glu Arg

657 666 675 684 693 702

AAG AAA TGG ATC CAT TGT TTC GAG AAC GTG ATC GCC CTC ATC TAC CTG GCC TCA

Lys Lys Trp Ile His Cys Phe Glu Asn Val Ile Ala Leu Ile Tyr Leu Ala Ser

711 720 729 738 747 756

CTG AGT GAA TAC GAC CAG TGC CTG GAG GAG AAC AAC CAG GAG AAC CGC ATG AAG

Leu Ser Glu Tyr Asp Gln Cys Leu Glu Glu Asn Asn Gln Glu Asn Arg Met Lys

765 774 783 792 801 810

GAG AGC CTC GCA TTG TTT GGG ACT ATC CTG GAA CTA CCC TGG TTC AAA AGC ACA

Glu Ser Leu Ala Leu Phe Gly Thr Ile Leu Glu Leu Pro Trp Phe Lys Ser Thr

819 828 837 846 855 864

TCC GTC ATC CTC TTT CTC AAC AAA ACC GAC ATC CTG GAG GAG AAA ATC CCC ACC

Ser Val Ile Leu Phe Leu Asn Lys Thr Asp Ile Leu Glu Glu Lys Ile Pro Thr

873 882 891 900 909 918

TCC CAC CTG GCT ACC TAT TTC CCC AGT TTC CAG GGC CCT AAG CAG GAT GCT GAG

Ser His Leu Ala Thr Tyr Phe Pro Ser Phe Gln Gly Pro Lys Gln Asp Ala Glu

927 936 945 954 963 972

GCA GCC AAG AGG TTC ATC CTG GAC ATG TAC ACG AGG ATG TAC ACC GGG TGC GTG

Ala Ala Lys Arg Phe Ile Leu Asp Met Tyr Thr Arg Met Tyr Thr Gly Cys Val

981 990 999 1008 1017 1026

GAC GGC CCC GAG GGC AGC AAG AAG GGC GCA CGA TCC CGA CGC CTT TTC AGC CAC

Asp Gly Pro Glu Gly Ser Lys Lys Gly Ala Arg Ser Arg Arg Leu Phe Ser His

1035 1044 1053 1062 1071 1080

TAC ACA TGT GCC ACA GAC ACA CAG AAC ATC CGC AAG GTC TTC AAG GAC GTG CGG

Tyr Thr Cys Ala Thr Asp Thr Gln Asn Ile Arg Lys Val Phe Lys Asp Val Arg

1089

1098

1107

1116

1125

GAC TCG GTG CTC GCC CGC TAC CTG GAC GAG ATC AAC AAC CTG CTG TGA

Asp Ser Val Leu Ala Arg Tyr Leu Asp Glu Ile Asn Leu Leu ***